

## STIC Biotechnology Systems Branch

### RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/550,498  
Source: PT/10  
Date Processed by STIC: 10/5/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

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## Raw Sequence Listing Error Summary

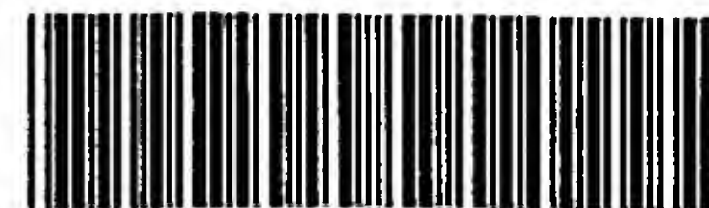
### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER: 10/550,498

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1        Wrapped Nucleics    The number/text at the end of each line "wrapped" down to the next line. This may occur if your file  
     Wrapped Aminos        was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will  
                               prevent "wrapping."
  
- 2        Invalid Line Length    The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
  
- 3        Misaligned Amino    The numbering under each 5<sup>th</sup> amino acid is misaligned. Do **not** use tab codes between numbers;  
     Numbering                use **space characters**, instead.
  
- 4        Non-ASCII            The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please**  
                               **ensure your subsequent submission is saved in ASCII text.**
  
- 5        Variable Length      Sequence(s)        contain n's or Xaa's representing more than one residue. **Per Sequence Rules,**  
                               **each n or Xaa can only represent a single residue.** Please present the **maximum** number of each  
                               residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6        PatentIn 2.0        A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
     "bug"                    sequences(s)       . Normally, PatentIn would automatically generate this section from the  
                               previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to  
                               the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for**  
                               **Artificial or Unknown sequences.**
  
- 7        Skipped Sequences    Sequence(s)        missing. If intentional, please insert the following lines for **each** skipped sequence:  
     (OLD RULES)            (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                               (i)        SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                               (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                               This sequence is intentionally skipped  
  
                               Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
  
- 8        Skipped Sequences    Sequence(s)        missing. If **intentional**, please insert the following lines for **each** skipped sequence.  
     (NEW RULES)            <210> sequence id number  
                               <400> sequence id number  
                               000
  
- 9        Use of n's or Xaa's    Use of n's and/or Xaa's have been detected in the Sequence Listing.  
     (NEW RULES)            Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.  
                               In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
  
- 10        Invalid <213>        Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or  
     Response                scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or  
                               is Artificial Sequence
  
- 11        Use of <220>        Sequence(s) 1-42 missing the <220> "Feature" and associated numeric identifiers and responses.  
                               Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or  
                               "Unknown." Please explain source of genetic material in <220> to <223> section.  
                               (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
  
- 12        PatentIn 2.0        Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,  
     "bug"                    resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence  
                               listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
  
- 13        Misuse of n/Xaa      "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



PCT

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/550,498

DATE: 10/05/2005

TIME: 16:19:28

Input Set : A:\persico.ST25.txt

Output Set: N:\CRF4\10052005\J550498.raw

3 <110> APPLICANT: Minchiotti, Gabriella  
 4       Persico, Maria  
 5       Parisi, Silvia  
 7 <120> TITLE OF INVENTION: METHOD FOR PROMOTING DIFFERENTIATION OF STAMINAL CELL  
 9 <130> FILE REFERENCE: 30242 PCT  
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/550,498  
 C--> 12 <141> CURRENT FILING DATE: 2005-09-20  
 14 <160> NUMBER OF SEQ ID NOS: 42  
 16 <170> SOFTWARE: PatentIn version 3.1  
 18 <210> SEQ ID NO: 1  
 19 <211> LENGTH: 22  
 20 <212> TYPE: DNA  
 21 <213> ORGANISM: Artificial  
 23 <220> FEATURE:  
 24 <221> NAME/KEY: primer\_bind  
 25 <222> LOCATION: (1)..(22)  
 26 <223> OTHER INFORMATION:  
 W--> 29 <400> 1  
 30 ttccttctca ggtcacgttt gc  
 33 <210> SEQ ID NO: 2  
 34 <211> LENGTH: 21  
 35 <212> TYPE: DNA  
 36 <213> ORGANISM: Artificial  
 38 <220> FEATURE:  
 39 <221> NAME/KEY: primer\_bind  
 40 <222> LOCATION: (1)..(21)  
 41 <223> OTHER INFORMATION:  
 W--> 44 <400> 2  
 45 ggtggggttg gtatcgtttc a  
 48 <210> SEQ ID NO: 3  
 49 <211> LENGTH: 25  
 50 <212> TYPE: DNA  
 51 <213> ORGANISM: Artificial  
 53 <220> FEATURE:  
 54 <221> NAME/KEY: primer\_bind  
 55 <222> LOCATION: (1)..(25)  
 56 <223> OTHER INFORMATION:  
 W--> 59 <400> 3  
 60 aaggatccag gctctgctgt gtgcc  
 63 <210> SEQ ID NO: 4  
 64 <211> LENGTH: 26  
 65 <212> TYPE: DNA  
 66 <213> ORGANISM: Artificial

pg 1-5

Does Not Comply  
Corrected Diskette Needed

This needs explanation on <223> line (see item 11 on ERM summary sheet)

← not an explanation

← same error

same

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Input Set : A:\persico.ST25.txt

Output Set: N:\CRF4\10052005\J550498.raw

68 <220> FEATURE:  
69 <221> NAME/KEY: primer\_bind  
70 <222> LOCATION: (1)..(26)  
71 <223> OTHER INFORMATION: *same*

W--> 74 <400> 4  
75 acggatccat gtccaacctc tggcgg 26  
78 <210> SEQ ID NO: 5  
79 <211> LENGTH: 20  
80 <212> TYPE: DNA  
81 <213> ORGANISM: Artificial  
83 <220> FEATURE:  
84 <221> NAME/KEY: primer\_bind  
85 <222> LOCATION: (1)..(20)  
86 <223> OTHER INFORMATION: *same*

W--> 89 <400> 5  
90 atgtgccgtg gtgtcgtggt 20  
93 <210> SEQ ID NO: 6  
94 <211> LENGTH: 20  
95 <212> TYPE: DNA  
96 <213> ORGANISM: Artificial  
98 <220> FEATURE:  
99 <221> NAME/KEY: primer\_bind  
100 <222> LOCATION: (1)..(20)  
101 <223> OTHER INFORMATION: *same*

W--> 104 <400> 6  
105 gacctcctga tcagggatac 20  
108 <210> SEQ ID NO: 7  
109 <211> LENGTH: 24  
110 <212> TYPE: DNA  
111 <213> ORGANISM: Artificial  
113 <220> FEATURE:  
114 <221> NAME/KEY: primer\_bind  
115 <222> LOCATION: (1)..(24)  
116 <223> OTHER INFORMATION: *same*

W--> 119 <400> 7  
120 gccagaagc ggatagaagg cggg 24  
123 <210> SEQ ID NO: 8  
124 <211> LENGTH: 24  
125 <212> TYPE: DNA  
126 <213> ORGANISM: Artificial  
128 <220> FEATURE:  
129 <221> NAME/KEY: primer\_bind  
130 <222> LOCATION: (1)..(24)  
131 <223> OTHER INFORMATION: *same*

W--> 134 <400> 8  
135 ctgtggttca gggctcagtc cttc 24  
138 <210> SEQ ID NO: 9  
139 <211> LENGTH: 24  
140 <212> TYPE: DNA



## RAW SEQUENCE LISTING

DATE: 10/05/2005

PATENT APPLICATION: US/10/550,498

TIME: 16:19:28

Input Set : A:\persico.ST25.txt

Output Set: N:\CRF4\10052005\J550498.raw

```

141 <213> ORGANISM: Artificial
143 <220> FEATURE:
144 <221> NAME/KEY: primer_bind
145 <222> LOCATION: (1)..(24)
146 <223> OTHER INFORMATION: same
W--> 149 <400> 9
150 ggaagagtga gcggcgcatc aagg 24
153 <210> SEQ ID NO: 10
154 <211> LENGTH: 22
155 <212> TYPE: DNA
156 <213> ORGANISM: Artificial
158 <220> FEATURE:
159 <221> NAME/KEY: primer_bind
160 <222> LOCATION: (1)..(22)
161 <223> OTHER INFORMATION: same
W--> 164 <400> 10
165 ctgctggaga gggtattcct cg 22
168 <210> SEQ ID NO: 11
169 <211> LENGTH: 25
170 <212> TYPE: DNA
171 <213> ORGANISM: Artificial
173 <220> FEATURE:
174 <221> NAME/KEY: primer_bind
175 <222> LOCATION: (1)..(25)
176 <223> OTHER INFORMATION: same
W--> 179 <400> 11
180 cctgctggat tacattaaag cactg 25
183 <210> SEQ ID NO: 12
184 <211> LENGTH: 25
185 <212> TYPE: DNA
186 <213> ORGANISM: Artificial
188 <220> FEATURE:
189 <221> NAME/KEY: primer_bind
190 <222> LOCATION: (1)..(25)
191 <223> OTHER INFORMATION: same
W--> 194 <400> 12
195 cctgaagtac tcattatagt caagg 25
198 <210> SEQ ID NO: 13
199 <211> LENGTH: 27
200 <212> TYPE: DNA
201 <213> ORGANISM: Artificial
203 <220> FEATURE:
204 <221> NAME/KEY: primer_bind
205 <222> LOCATION: (1)..(27)
206 <223> OTHER INFORMATION: same
W--> 209 <400> 13
210 gtaagtcgct tattaaaact tgctgctc 27
213 <210> SEQ ID NO: 14
214 <211> LENGTH: 27

```

## RAW SEQUENCE LISTING

DATE: 10/05/2005

PATENT APPLICATION: US/10/550,498

TIME: 16:19:28

Input Set : A:\persico.ST25.txt

Output Set: N:\CRF4\10052005\J550498.raw

215 <212> TYPE: DNA  
 216 <213> ORGANISM: Artificial  
 218 <220> FEATURE:  
 219 <221> NAME/KEY: primer\_bind  
 220 <222> LOCATION: (1)..(27)  
 221 <223> OTHER INFORMATION: *same*  
 W--> 224 <400> 14  
 225 gacagcaagt tttaataagc gacttac 27  
 228 <210> SEQ ID NO: 15  
 229 <211> LENGTH: 38  
 230 <212> TYPE: DNA  
 231 <213> ORGANISM: Artificial  
 233 <220> FEATURE:  
 234 <221> NAME/KEY: primer\_bind  
 235 <222> LOCATION: (1)..(38)  
 236 <223> OTHER INFORMATION: *same*  
 W--> 239 <400> 15  
 240 cttgctgtct gaatggaaac acttgcaccc tgggggtcc 38  
 243 <210> SEQ ID NO: 16  
 244 <211> LENGTH: 38  
 245 <212> TYPE: DNA  
 246 <213> ORGANISM: Artificial  
 248 <220> FEATURE:  
 249 <221> NAME/KEY: primer\_bind  
 250 <222> LOCATION: (1)..(38)  
 251 <223> OTHER INFORMATION: *same*  
 W--> 254 <400> 16  
 255 ggaccccagg atgcaagtgt ttccattcag acagcaag 38  
 258 <210> SEQ ID NO: 17  
 259 <211> LENGTH: 23  
 260 <212> TYPE: DNA  
 261 <213> ORGANISM: Artificial  
 263 <220> FEATURE:  
 264 <221> NAME/KEY: primer\_bind  
 265 <222> LOCATION: (1)..(23)  
 266 <223> OTHER INFORMATION: *same*  
 W--> 269 <400> 17  
 270 gaatggaggg gcttgcaccc tgg 23  
 273 <210> SEQ ID NO: 18  
 274 <211> LENGTH: 23  
 275 <212> TYPE: DNA  
 276 <213> ORGANISM: Artificial  
 278 <220> FEATURE:  
 279 <221> NAME/KEY: primer\_bind  
 280 <222> LOCATION: (1)..(23)  
 281 <223> OTHER INFORMATION: *same*  
 W--> 284 <400> 18  
 285 ccaggatgca agcccctcca ttc 23  
 288 <210> SEQ ID NO: 19

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/550,498

DATE: 10/05/2005

TIME: 16:19:28

Input Set : A:\persico.ST25.txt

Output Set: N:\CRF4\10052005\J550498.raw

289 <211> LENGTH: 29  
 290 <212> TYPE: DNA  
 291 <213> ORGANISM: Artificial  
 293 <220> FEATURE:  
 294 <221> NAME/KEY: primer\_bind  
 295 <222> LOCATION: (1)..(29)  
 296 <223> OTHER INFORMATION: *same*  
 W--> 299 <400> 19  
 300 cttgcatcct gggggccttc tgtgcctgc 29  
 303 <210> SEQ ID NO: 20  
 304 <211> LENGTH: 29  
 305 <212> TYPE: DNA  
 306 <213> ORGANISM: Artificial  
 308 <220> FEATURE:  
 309 <221> NAME/KEY: primer\_bind  
 310 <222> LOCATION: (1)..(29)  
 311 <223> OTHER INFORMATION: *same*  
 W--> 314 <400> 20  
 315 gcaggcacag aaggccccca ggatgcaag 29  
 318 <210> SEQ ID NO: 21  
 319 <211> LENGTH: 31  
 320 <212> TYPE: DNA  
 321 <213> ORGANISM: Artificial  
 323 <220> FEATURE:  
 324 <221> NAME/KEY: primer\_bind  
 325 <222> LOCATION: (1)..(31)  
 326 <223> OTHER INFORMATION: *same*  
 W--> 329 <400> 21  
 330 gcacccctggg gtccgcctgt gcctgcctc c 31  
 333 <210> SEQ ID NO: 22  
 334 <211> LENGTH: 31  
 335 <212> TYPE: DNA  
 336 <213> ORGANISM: Artificial  
 338 <220> FEATURE:  
 339 <221> NAME/KEY: primer\_bind  
 340 <222> LOCATION: (1)..(31)  
 341 <223> OTHER INFORMATION: *same*  
 W--> 344 <400> 22  
 345 gcacccctggg gtccgcctgt gcctgcctc c 31  
 348 <210> SEQ ID NO: 23  
 349 <211> LENGTH: 31  
 350 <212> TYPE: DNA  
 351 <213> ORGANISM: Artificial  
 353 <220> FEATURE:  
 354 <221> NAME/KEY: primer\_bind  
 355 <222> LOCATION: (1)..(31)  
 356 <223> OTHER INFORMATION: *same*  
 W--> 359 <400> 23  
 360 gcacccctggg gtccgcctgt gcctgcctc c

FYI (global error)  
 The types of errors shown exist throughout  
 the Sequence Listing. Please check subsequent  
 sequences for similar errors.

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/550,498

DATE: 10/05/2005  
TIME: 16:19:29

Input Set : A:\persico.ST25.txt  
Output Set: N:\CRF4\10052005\J550498.raw

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,  
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27  
Seq#:28,29,30,31,32,33,34,35,36,37,38,39,40,41,42



## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/550,498

DATE: 10/05/2005

TIME: 16:19:29

Input Set : A:\persico.ST25.txt

Output Set: N:\CRF4\10052005\J550498.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:29 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:26  
L:44 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:41  
L:59 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:56  
L:74 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:71  
L:89 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:86  
L:104 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:101  
L:119 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:116  
L:134 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:131  
L:149 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:146  
L:164 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:10,Line#:161  
L:179 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11,Line#:176  
L:194 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:12,Line#:191  
L:209 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:13,Line#:206  
L:224 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:14,Line#:221  
L:239 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:15,Line#:236  
L:254 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:16,Line#:251  
L:269 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:17,Line#:266  
L:284 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:18,Line#:281  
L:299 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:19,Line#:296  
L:314 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:20,Line#:311  
L:329 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:21,Line#:326  
L:344 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:22,Line#:341  
L:359 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:23,Line#:356  
L:374 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:24,Line#:371  
L:389 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:25,Line#:386  
L:404 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:26,Line#:401  
L:419 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:27,Line#:416  
L:434 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:28,Line#:431  
L:449 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:29,Line#:446  
L:464 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:30,Line#:461  
L:479 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:31,Line#:476  
L:494 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:32,Line#:491  
L:509 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:33,Line#:506  
L:566 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:34,Line#:563  
L:619 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:35,Line#:616  
L:676 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:36,Line#:673  
L:725 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:37,Line#:722  
L:774 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:38,Line#:771  
L:807 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:39,Line#:804  
L:844 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:40,Line#:841  
L:905 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:41,Line#:902  
L:962 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:42,Line#:959

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